



1 AGATGAGTGT GGGGGGTGGA AGAGTCAAGT TGCTGGGCAT
METSerVal GlyArgArg ArgValLysLeu LeuGlyIle
41 CCTGATGATG GCAAATGTCT TCATTTATTT GATTIGGGAA
eLeuMETMET AlaAsnValPhe IleTyrLeu IleValGlu
81 GTCTCCAAAA ACAGTAGCCA AGACAAAAAT GGAAAGGGAG
ValSerLysAsn SerSerGln AspLysAsn GlyLysGlyG
121 GAGTAATAAT CCGAAAGAG AAGTTCTGGA AGCCACCAG
lyValIleIle ProLysGlu LysPheTrpLys ProProSe
161 CACTCCCCCG GCATACTGGA ACAGGGAACA GGAGAAGCTG
rThrProArg AlaTyrTrpAsn ArgGluGln GluLysLeu
201 AACAGGTGGT ACAATCCCAT CTGGAACAGG GTGGCCAATC
AsnArgTrpTyr AsnProIle LeuAsnArg ValAlaAsnG
241 AGACAGGGGA GCTAGCCACA TCTCCAAACA CAAGTCACCT
InThrGlyGlu LeuAlaThr SerProAsnThr SerHisLe
281 GAGCTATTGT GAACAGACT CGACGGTCAT GACAGCTGTG
uSerTyrCys GluProAspSer ThrValMET ThrAlaVal
321 ACAGATTTTA ATAATCTGCC GGACAGATTT AAAGACTTTC
ThrAspPheAsn AsnLeuPro AspArgPhe LysAspPheL
361 TCTTGTAATTT GAGATGGCCG AATTACTGCC TGCTTATAGA
eLeuTyrLeu ArgCysArg AsnTyrSerLeu LeuIleAs
401 TCAACCGAAG AAATGTGCAA AGAAGCCCTT CTACTATTG
pGlnProLys LysCysAlaLys LysProPhe LeuLeuLeu
441 GCGATAAAGT CCTCATTC ACATTTTGCC AGAAGGCAAG
AlaIleLysSer LeuIlePro HisPheAla ArgArgGlnA
481 CAATTGGGA GTCTTGGGGC CGAGAAACCA ACGTAGGGAA
laIleArgGlu SerTrpGly ArgGluThrAsn ValGlyAs
521 CCAGACAGTA GTGAGGGTCT TCTGTGTGG CAAGACACCC
nGlnThrVal ValArgValPhe LeuLeuGly LysThrPro
561 CCAGAGGACA ACCACCTGA CCTTTGGGAC ATGCTTAAGT
ProGluAspAsn HisProAsp LeuSerAsp METLeuLysP
601 TTGAGAGTGA CAAGCACCCAG GACATCCTCA TGIGGAACTA
heGluSerAsp LysHisGln AspIleLeuMET TrpAsnTy
641 TAGAGACACA TTCTTCAACC TGTCCTGAA GGAAGTCTG
rArgAspThr PhePheAsnLeu SerLeuLys GluValLeu

FIG. 1A

681 TTCTTAGGT GGGTGGCAC TTCTGTCCA GAGGAGAGT
 PheLeuArgTrp ValSerThr SerCysPro AspAlaGluP
 721 TTGCTTCAA GGGGATGAT GAAGGTTTG TGAACACCA
 heValPheLys GlyAspAsp AspValPheVal AsnThrHi
 761 TCACATCCTT AATTACTTGA ATAGCTTATC CAAGAGCAA
 sHisIleLeu AsnTyrLeuAsn SerLeuSer LysSerLys
 801 GCCAAGACT TGTTCATAGG TGAAGTATC CACAATGCTG
 AlaLysAspLeu PheIleGly AspValIle HisAsnAlaG
 841 GGCTCACC GGATAAGAAA CTGAAGTACT ACATCCAGA
 lyProHisArg AspLysLys LeuLysTyrTyr IleProGl
 881 AGTCTTCTAC ACCGGGCTCT ACCCACCCTA TCCCGGGGT
 uValPheTyr ThrGlyValTyr ProProTyr AlaGlyGly
 921 GGTCATTC TGTACTCCG CCCCCTTGGC TTGAGGCTGT
 GlyGlyPheLeu TyrSerGly ProLeuAla LeuArgLeuT
 961 ACAGTGGAC TAGCCCGGTC CATCTCTACC CTATTGATGA
 yrSerAlaThr SerArgVal HisLeuTyrPro IleAspAs
 1001 TGTTTATAC GGAATGTGGC TTCAGAACT GGGCTTGT
 pValTyrThr GlyMETCysLeu GlnLysLeu GlyLeuVal
 1041 CCAGAGAAGC ACAAAGGCTT CAGGACATTT GATATTGAAG
 ProGluLysHis LysGlyPhe ArgThrPhe AspIleGluG
 1081 AGAAAAATAA GAAAAATATT TGTTCCTATA TAGACCTAAT
 luLysAsnLys LysAsnIle CysSerTyrIle AspLeuME
 1121 GTTAGTACAT AGCAGAAAC CTCAAGAGAT GATTGATATC
 TLeuValHis SerArgLysPro GlnGluMET IleAspIle
 1161 TGGTCTCAGT TGCAAAGTCC TAATTTAAAA TGCTGA
 TrpSerGlnLeu GlnSerPro AsnLeuLys Cys

FIG. 1B

MAX - RRKV - - - - - LLR - LL - - V
 10 20 30
 MSVG R - - - - - KL
 MA - - S SC - - - - - Y - - - - -
 MAP - - - - - AVL TALPNRMS S S KWSL
 MQSKH RFL - - - - - C L - - - - -
 MLQW R RHCCFAKMTWNAKRS F TH IG
 LSLVXLXXXFXFLXH - - W - - - - -
 40 50 60
 LGILMMANV IY IVEVSKNSSQDKNGKGG
 LSVVC - - - - - ASA - - - - -
 L - - - - - LSLLS V - - - - -
 LPLILLVDYCGLT LHL - - - - -
 LSLVFLFAM L FNL HD L PGRAGFKENPV
 - - - F - - - F - - P - - - - - IWY
 70 80 90
 VIIPKEK WK PSTPRAYWNREQEKLNRWY
 - - - - - - - - - - - - - - - - LWY
 - - - - - - - - - - - - - - - - LWY
 ELNFERH HY - - - - - - - - - -
 TYTFERG RSTKSETNHSSLR - - - - - NIWK
 LSIP - - LRPQTGSXSXSXXLSHL - Y - - - - N
 100 110 120
 NPILNRVAN T ELAT PNT SHLSVCEPDS
 LSIT - - - - - S YTG KPF SHI - - - - -
 LSLPHY - - - - - - - - - - - - -
 - - - - - LND D G A S G D K F A - - - - -
 ETV PQT L P P O T A T N N N T D P Q G V T G L E N
 TVXRNXNXFXNNXXTR - - - - - PINSXXFEF
 130 140 150
 TVMTAVTD FNNLPDF FKDFLLYLRCRNYSL
 TVAKKNFT FGMIRPP - - - - - PINPHSFFF
 VIERV NWMYF - YEYE - - - - - PIYRQDFRF
 - - - - - - - - - - - - - - - - LRVPSFTAEV
 T L S A N G S I Y N E K G T G - - - - - H P N S Y H E K Y
 LIDEPXKCXKK - PFLVLLIKSXPGXFXARQ
 160 170 180

FIG. 2A

160 170 180
 L I P Q I K A - L A L I P H A R
 L I N N E N I I S T H K E D
 T L R H S N S H Q N I V T R S D V K
 P V Q A R - - - T M A V N S R R E
 I N E Q E S I A A E Q I E R
 A I R E T W G X E X N F X G I X V X R V F L L G K X A - E X
 190 200 210
 A I R E S W G R E T N V G N O T V V F L L G Q T P P D
 A I R E T W G D E N H K K I A T L F L L G N A - -
 A I F V T W G E K K S W W C Y E M L T F F L L G Q Q A - F R
 A I F R T W G Y E G R S D V H L R V F L L G T A E D S E
 A I F Q T W G N F S L A P Q I T F I F L L G L S I - - K
 X D P X L X X M V E X E S R X H G D I I Q Q D F L D T Y F N
 220 230 240
 N H D L S D M L K F E S D K Q D I L M W N Y R D F F H
 - C F V L N Q M V E Q E S Q I F H D I I V E D F I C S Y H
 E C K T A L S L F D E H V L Y S D I R D D F L D T Y N
 K - - - - A W E S H E H G D I L A D F T C A Y F N
 L N G Y I Q R A I L E E S P Q Y H D I I Q C E Y D D T Y Y
 L T L K T L M G M R W V A T F C P X A E Y V M K T D S D V F
 250 260 270
 S L K E V L F L R W V S I S I D A F F F G I D D Y F
 L L K T L M G R W V A T F C P X A E Y V M K T D S D V F
 T L K T I M A F R W V M E C I N K Y I M K T D T D V F
 N T L K T M L G M R W A S E Q F N R S F Y L F V L D D Y Y
 T I K T L M G M N R V A T Y H I P Y V M K T D S D V F
 V N T X N L L N K L L K P S L S H R X X L F T G Y - V I X G
 280 290 300
 N T H H I L N Y L N S L K K A K D F I S - D V I H N
 M D N L I Y L L F F F T K P R R Y F T G Y - V I N
 I T G N I V K Y L - - N N S E K F F T G Y P L D N
 S A K M V I K F L G R G R Q O P E L F A G H V F Q T
 N T E Y L I N F L I F D P P H N Y F T G Y - L M R

FIG. 2B

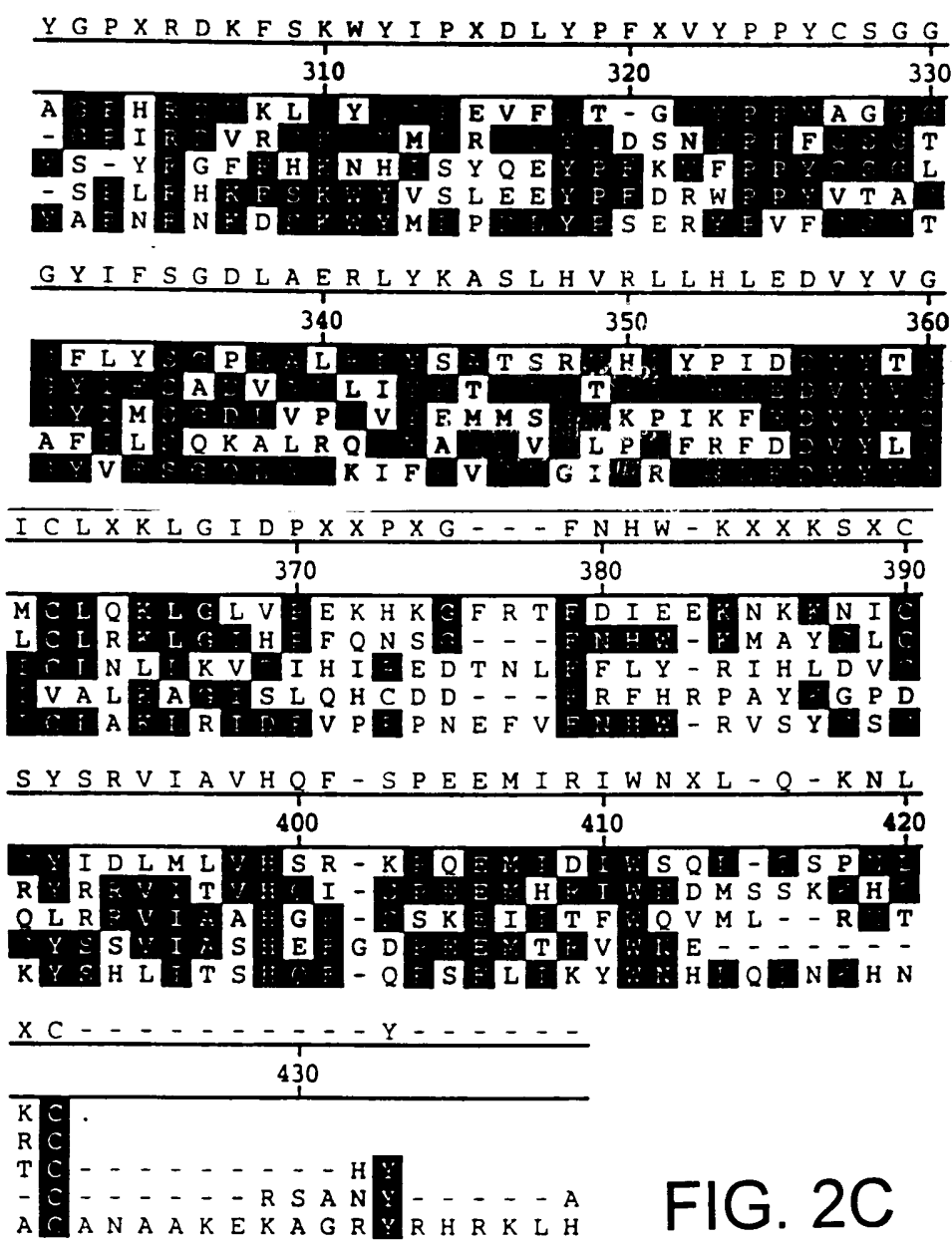


FIG. 2C

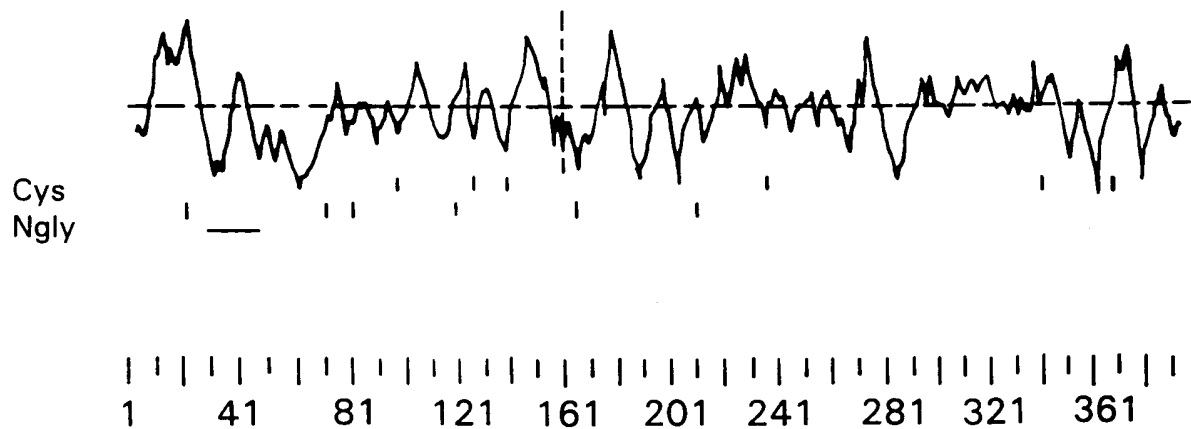


FIG. 3

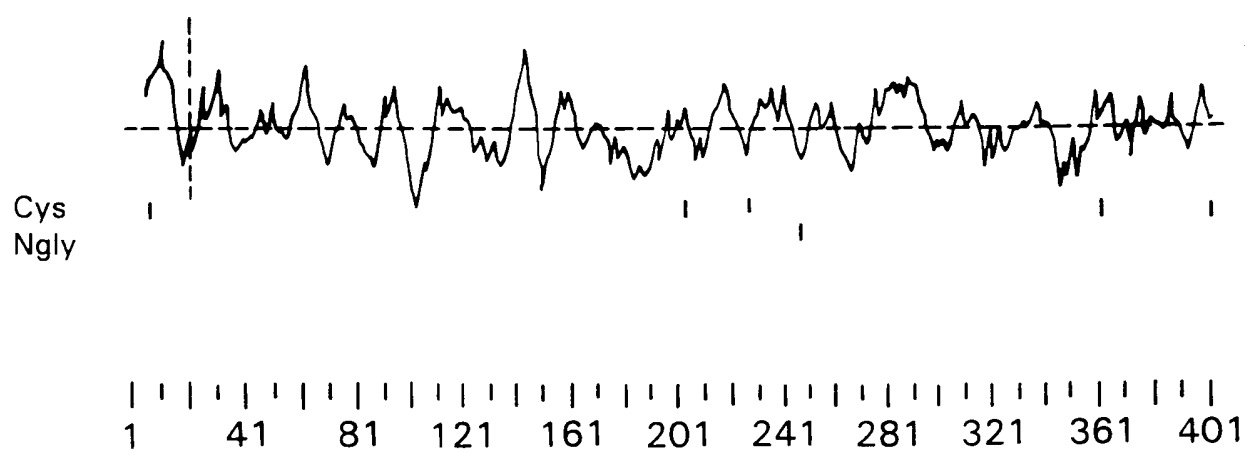


FIG. 5

1 ATGATTTGCC CTCAGCTTT ACTGGTTATT TTAAGAAATT
METIleCysPro SerAlaLeu LeuValIle LeuArgAsnL
41 TAATACGGGA AGAAAAATC ATTTCTCAAG AGATCCTCAA
euIleArgGlu GluLysIle IleSerGlnGlu IleLeuAs
81 TTTGATTGAA TTAAGGATGA AAAAAGGGAA TATTTCAGTTG
nLeuIleGlu LeuArgMETLys LysGlyAsn IleGlnLeu
121 ACAACTCTG CAATCAGTGA TGCATTAAAA GAAATCGATA
ThrAsnSerAla IleSerAsp AlaLeuLys GluIleAspS
161 GTAGTGTGCT CAATGTTCCT GTCACCGGGG AGACGGGATC
erSerValLeu AsnValAla ValThrGlyGlu ThrGlySe
201 AGGGAAGTCC AGCTTCATCA ATAOCCTGAG AGGCATTGGG
rGlyLysSer SerPheIleAsn ThrLeuArg GlyIleGly
241 AATGAAGAAG AAGGTGCAGC TAAACTGGG GTGGTGGAGG
AsnGluGluGlu GlyAlaAla LysThrGly ValValGluV
281 TAACCATGGA AAGACATCCA TACAAACACC OCAATATAACC
alThrMETGlu ArgHisPro TyrLysHisPro AsnIlePr
321 CAATGIGGTT TTTTGGGACC TGCCCTGGGAT TGGAAGCACA
oAsnValVal PheTrpAspLeu ProGlyIle GlySerThr
361 AATTTCOCAC CAAACACTTA OCTGGAGAAA ATGAAGTTCT
AsnPheProPro AsnThrTyr LeuGluLys METLysPheT
401 ATGAGTACGA TTCTCTCATT ATTATTTCGG CCACACGCTT
yrGluTyrAsp PhePheIle IleIleSerAla ThrArgPh
441 CAAGAAAAAT GATATAGACA TTGCCAAAGC AATCAGCATG
eLysLysAsn AspIleAspIle AlaLysAla IleSerMET
481 ATGAAGAAGG AATTCTACTT CGTGAGAAOC AAGGTGGACT
METLysLysGlu PheTyrPhe ValArgThr LysValAspS
521 CTGACATAAC AAATGAAGCA GATGGCAAAC CTCAAACCTT
erAspIleThr AsnGluAla AspGlyLysPro GlnThrPh
561 TGACAAAGAA AAGGTCTGCG AGGACATCCG CCTTAACTGT
eAspLysGlu LysValLeuGln AspIleArg LeuAsnCys
601 GTGAACACCT TTAGGGAGAA TGGCATTGCT GAGCCACCAA
ValAsnThrPhe ArgGluAsn GlyIleAla GluProProI
641 TCTTCTGCT CTCTAACAAA AATGTTTIGTC ACTATGACTT
lePheLeuLeu SerAsnLys AsnValCysHis TyrAspPh

FIG. 4A

681 CCCCCTCCTG ATGGACAAGC TGATAAGTGA CCTCCTATC
eProValLeu METAspLysLeu IleSerAsp LeuProIle
721 TACAGGAGAC ACAATTTTAT GGTCTCCTTA CCAATATCA
TyrArgArgHis AsnPheMET ValSerLeu ProAsnIleT
761 CAGATTCAGT CATTGAAAAG AAGCGGCAAT TTCTGAAGCA
hrAspSerVal IleGluLys LysArgGlnPhe LeuLysGl
801 RAGGATTTGG CTGGAAGGAT TTCTGCTGA OCTAGTGAAT
nArgIleTrp LeuGluGlyPhe AlaAlaAsp LeuValAsn
841 ATCATCCTT CTCTGACCTT TCCTCTGGAC AGTGAATTGG
IleIleProSer LeuThrPhe LeuLeuAsp SerAspLeuG
881 AGACTCTGAA GAAAAGCATG AAATTCCTACC GCACTGTGTT
luThrLeuLys LysSerMET LysPheTyrArg ThrValPh
921 TGGAGTGGAT GAAACATCTT TGCAGAGATT AGCTAGGGAC
eGlyValAsp GluThrSerLeu GlnArgLeu AlaArgAsp
961 TGGGAAATAG AGGTGGATCA GGTGGAGGCC ATGATAAAAT
TrpGluIleGlu ValAspGln ValGluAla METIleLysS
1001 CTCCTGCTGT GTTCAAACCT ACAGATGAAG AAACAATACA
erProAlaVal PheLysPro ThrAspGluGlu ThrIleGl
1041 AGAAAGGCCT TCAAGATATA TTCAGGAGTT CIGTTTGGCT
nGluArgLeu SerArgTyrIle GlnGluPhe CysLeuAla
1081 AATGGGTACT TACTTCTTAA AAATAGTTTT CTAAAGAAA
AsnGlyTyrLeu LeuProLys AsnSerPhe LeuLysGluI
1121 TATTTTAOCT GAAATATTAT TTCCTTGACA TGGTGACTGA
lePheTyrLeu LysTyrTyr PheLeuAspMET ValThrGl
1161 GGATGCTAAA ACTCTTCTTA AAGAGATATG TTTAAGAAAC
uAspAlaLys ThrLeuLeuLys GluIleCys LeuArgAsn
1201 TAG

FIG. 4B

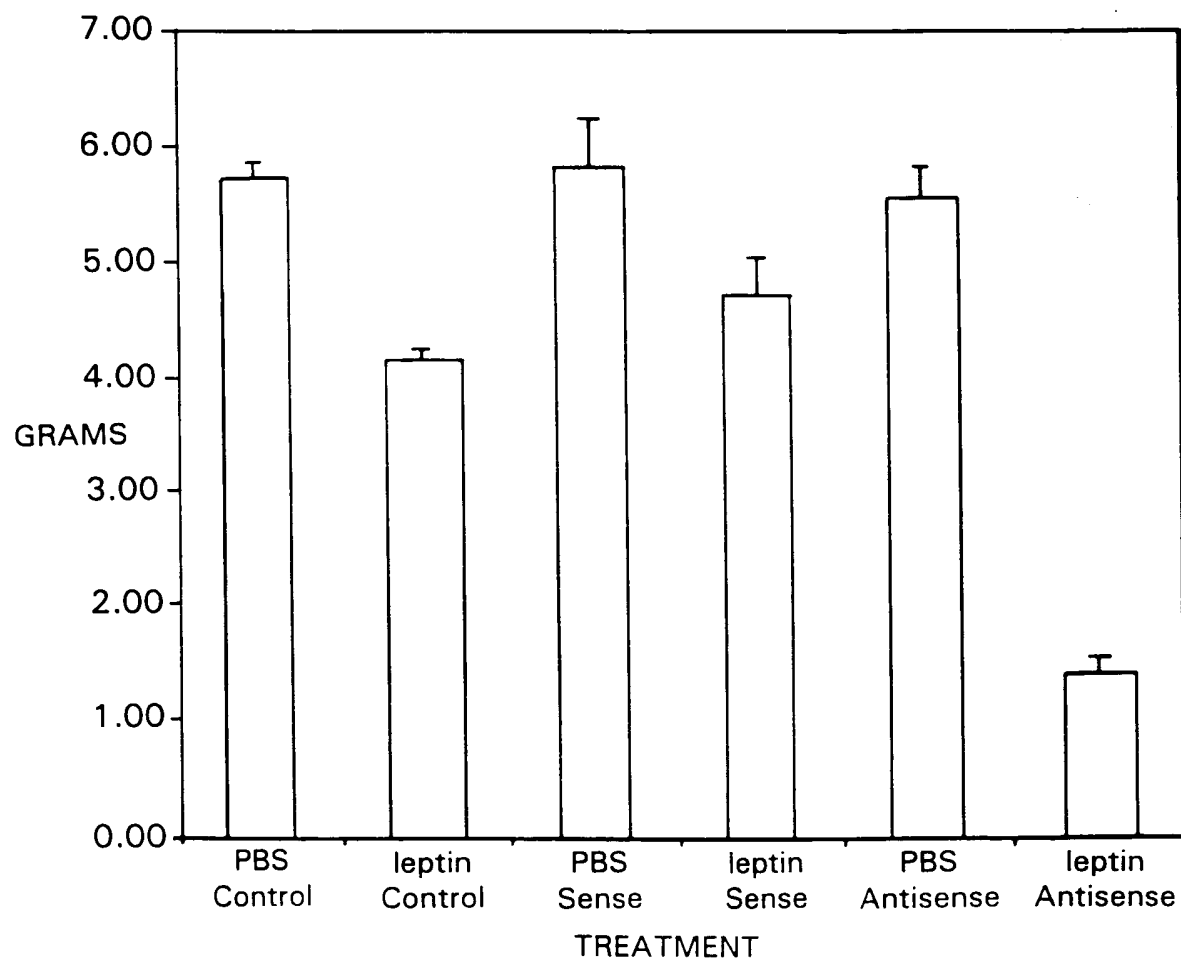


FIG. 6

5'

ACGCGTCCGCGCAGCGGCAGCGGCAGCAGCGGCAACAAGTGCCGGAGGCTA
GCAGAGCCAAGCCGGAGCAGTCCCTGCCGCCGACACCGCCGGGGCCCGCCGTC
CGGGGCGCCGCGCATGGAGCGTGAGCTGCGGGCGGTGCGCCGGGCTGAGCCGC
GCGGAGCGGGCCGGGACGTGGATGTGGCCGCGATCTCCCGCCCTTGCCCCCGC
CCCGCCGAGCTGGAGCTGCTCCCGGACAAGATATGAGAAATGAGTGTTGGA
CGTCGAAGAATAAAGTTGTTGGGTATCCTGATGATGGCAAATGTCTTCATTTA
TTTTATTATGGAAGTCTCCAAAAGCAGTAGCCAAGAAAAAAATGGAAAAGGG
GAAGTAATAATACCCAAAGAGAAGTTCTGGAAGATATCTACCCCTCCCGAGG
CATACTGGAACCGAGAGCAAGAGAAGCTGAACCGGCAGTACAACCCCATCCT
GAGCATGCTGACCAACCAGACGGGGGAGGCGGGCAGGCTCTCCAATATAAG
CCATCTGAACTACTGCGAACCTGACCTGAGGGTCACGTCGGTGGTTACGGGT
TTTAACAACCTTGCCGGACAGATTTAAAGACTTTCTGCTGTATTTGAGATGCCG
CAATTATTCACTGCTTATAGATCAGCCGGATAAGTGTGCAAAGAAACCTTTCT
TGTTGCTGGCGATTAAAGTCCCTCACTCCACATTTTGCCAGAAGGCAAGCAATC
CGGGAATCCTGGGGCCAAGAAAGCAACGCAGGGAACCAACCGGTGGTGCGA
GTCTTCCTGCTGGGCCAGACACCCCCAGAGGACAACCACCCCGACCTTTCAG
ATATGCTGAAATTTGAGAGTGAGAAGCACCAAGACATTCTTATGTGGAACTA
CAGAGACACTTTCTTCAACTTGTCTCTGAAGGAAGTGCTGTTTCTCAGGTGGG
TAAGTACTTCCTGCCCAGACACTGAGTTTGTTCCTCAAGGGCGATGACGATGTT
TTTGTGAACACCCATCACATCCTGAATTACTTGAATAGTTTATCCAAGACCAA
AGCCAAAGATCTCTTCATAGGTGATGTGATCCACAATGCTGGACCTCATCGG
GATAAGAAGCTGAAGTACTACATCCCAGAAGTTGTTTACTCTGGCCTCTACCC
ACCCTATGCAGGGGGAGGGGGGTTCTCTACTCCGGCCACCTGGCCCTGAGG
CTGTACCATATCACTGACCAGGTCCATCTCTACCCCATTGATGACGTTTATAC
TGGAATGTGCCTTCAGAACTCGGCCTCGTTCCAGAGAAACACAAAGGCTTC

FIG. 7A

AGGACATTTGATATCGAGGAGAAAAACAAAAATAACATCTGCTCCTATGTAG
ATCTGATGTTAGTACATAGTAGAAAACCTCAAGAGATGATTGATATTTGGTCT
CAGTTGCAGAGTGCTCATTTAAAATGCTAAAATAGATACAACTCAATTTKG
SATWGRAAGGGGTWTTTTGRATWGGYCCCATGTTGGGGTCTCACATTAGAGT
AATTTCTATTTNAANCATGAAATTGCCTTTATGAGTGATACCCATTTANGGCC
TCTAANCCTTCATTTGNACTCACGTGAAGAAGCGGAAAGCGGGAGAAGGTAAT
TTNTTTATGGTGAATGGCAGGATATTGGTCTGACTTACCGNTAGGGGANTTTA
AAACTGGNCCTTTTTGAATCTGTTTGGATGGCCCTT

FIG. 7B

MSVGRRRIKLLGILMMANVFIYFIMEVSKSSSQEKNGKGEVIIPKEKFWKISTPPE
AYWNREQEKLNRQYNPILSMLTNQTGEAGRLSNISHLNYCEPDLRVTSVVTGFN
NLPDRFKDFLLYLRCRNYSLLIDQPDKCAKKPFLLLAIKSLTPHFARRQAIRESWG
QESNAGNQTVVRVFLLGQTPPEDNHPDLSDMLKFESEKHQDILMWNRYRDTFFNL
SLKEVLFLRWVSTSCPDTEFVFKGDDDVFNTHHILNYLNSLSKTKAKDLFIGDV
IHNAGPHRDKKLKYYPEVVYSGLYPPYAGGGGFLYSGHLALRLYHITDQVHLY
PIDDVYTGMCLQKLGLVPEKHKGFRTFDIEEKNKNNICSYVDLMLVHSRKPQEM
IDIWSQLQSAHLKC

FIG. 8

246 ATGAGTGTGGACGTCGAAGAATAAAGTTGTTG--GG-TATCCTGATGATGGCAAATGTC 302
 |||||||||||||||||||||||||||| || ||||||||||||||||||||
 1 ATGAGTGTGGACGTCGAAGAATAAAGTTGTTGTTGGGTATCCTGATGATGGCAAATGTC 60

 303 TTCATTTATTTTATTATGGAAGTCTCCAAAAGCAGTAGCCAAGAAAAAATGGAAAAGGG 362
 ||||||||||||||||||||||||||||||||||||||||||||||||
 61 TTCATTTATTTTATTATGGAAGTCTCCAAAAGCAGTAGCCAAGAAAAAATGGAAAAGGG 120

 363 GAAGTAATAATACCCAAAGAGAAGTTCTGGAAGATATCTACCCCTCCCAGGCATACTGG 422
 ||||||||||||||||||||||||||||||||||||||||||||||||
 121 GAAGTAATAATACCCAAAGAGAAGTTCTGGAAGATATCTACCCCTCCCAGGCATACTGG 180

 423 AACCGAGAGCAAGAGAAGCTGAACCGGCAGTACAACCCCATCCTGAGCATGCTGACCAAC 482
 ||||||||||||||||||||||||||||||||||||||||||||||||
 181 AACCGAGAGCAAGAGAAGCTGAACCGGCAGTACAACCCCATCCTGAGCATGCTGACCAAC 240

 483 CAGACGGGGGAGGCGGGCAGGCTCTCCAATATAAGCCATCTGAACTACTGCGAACCTGAC 542
 ||||||||||||||||||||||||||||||||||||||||||||||||
 241 CAGACGGGGGAGGCGGGCAGGCTCTCCAATATAAGCCATCTGAACTACTGCGAACCTGAC 300

 543 CTGAGGGTCACGTCGGTGGTTACGGGTTTTAACAACCTTGCCGGACAGATTTAAAGACTTT 602
 ||||||||||||||||||||||||||||||||||||||||||||||||
 301 CTGAGGGTCACGTCGGTGGTTACGGGTTTTAACAACCTTGCCGGACAGATTTAAAGACTTT 360

 603 CTGCTGTATTTGAGATGCCGCAATTATTCAGTCTTATAGATCAGCCGGATAAGTGTGCA 662
 ||||||||||||||||||||||||||||||||||||||||||||||||
 361 CTGCTGTATTTGAGATGCCGCAATTATTCAGTCTTATAGATCAGCCGGATAAGTGTGCA 420

 663 AAGAAACCTTTCTTGTTGCTGGCGATTAAGTCCCTCACTCCACATTTTGCCAGAAGGCAA 722
 ||||||||||||||||||||||||||||||||||||||||||||||||
 421 AAGAAACCTTTCTTGTTGCTGGCGATTAAGTCCCTCACTCCACATTTTGCCAGAAGGCAA 480

 723 GCAATCCGGGAATCCTGGGGCCAAGAAAGCAACGCAGGGAACCAAACGGTGGTGCGAGTC 782
 ||||||||||||||||||||||||||||||||||||||||||||||||
 481 GCAATCCGGGAATCCTGGGGCCAAGAAAGCAACGCAGGGAACCAAACGGTGGTGCGAGTC 540

 783 TTCCTGCTGGGCCAGACACCCCCAGAGGACAACCACCCGACCTTTCAGATATGCTGAAA 842
 ||||||||||||||||||||||||||||||||||||||||||||||||

FIG. 9A

541 TTCCTGCTGGGCCAGACACCCCCAGAGGACAACCACCCCGACCTTTCAGATATGCTGAAA 600
 843 TTTGAGAGTGAGAAGCACCAAGACATTCTTATGTGGAACCTACAGAGACACTTTCTTCAAC 902
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 601 TTTGAGAGTGAGAAGCACCAAGACATTCTTATGTGGAACCTACAGAGACACTTTCTTCAAC 660
 903 TTGTCTCTGAAGGAAGTGCTGTTTCTCAGGTGGGTAAGTACTTCCTGCCCAGACACTGAG 962
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 661 TTGTCTCTGAAGGAAGTGCTGTTTCTCAGGTGGGTAAGTACTTCCTGCCCAGACACTGAG 720
 963 TTTGTTTTCAAGGGCGATGACGATGTTTTTGTGAACACCCATCACATCCTGAATTACTTG 1022
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 721 TTTGTTTTCAAGGGCGATGACGATGTTTTTGTGAACACCCATCACATCCTGAATTACTTG 780
 1023 AATAGTTTATCCAAGACCAAAGCCAAAGATCTCTTCATAGGTGATGTGATCCACAATGCT 1082
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 781 AATAGTTTATCCAAGACCAAAGCCAAAGATCTCTTCATAGGTGATGTGATCCACAATGCT 840
 1083 GGACCTCATCGGGATAAGAAGCTGAAGTACTACATCCCAGAAGTTGTTTACTCTGGCCTC 1142
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 841 GGACCTCATCGGGATAAGAAGCTGAAGTACTACATCCCAGAAGTTGTTTACTCTGGCCTC 900
 1143 TACCCACCCTATGCAGGGGGAGGGGGGTTCTCTACTCCGGCCACCTGGCCCTGAGGCTG 1202
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 901 TACCCACCCTATGCAGGGGGAGGGGGGTTCTCTACTCCGGCCACCTGGCCCTGAGGCTG 960
 1203 TACCATATCACTGACCAGGTCCATCTCTACCCCATGATGACGTTTATACTGGAATGTGC 1262
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 961 TACCATATCACTGACCAGGTCCATCTCTACCCCATGATGACGTTTATACTGGAATGTGC 1020
 1263 CTTCAGAAACTCGGCCTCGTTCCAGAGAAACACAAAGGCTTCAGGACATTTGATATCGAG 1322
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1021 CTTCAGAAACTCGGCCTCGTTCCAGAGAAACACAAAGGCTTCAGGACATTTGATATCGAG 1080
 1323 GAGAAAAACAAAAATAACATCTGCTCCTATGTAGATCTGATGTTAGTACATAGTAGAAAA 1382
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1081 GAGAAAAACAAAAATAACATCTGCTCCTATGTAGATCTGATGTTAGTACATAGTAGAAAA 1140
 1383 CCTCAAGAGATGATTGATATTTGGTCTCAGTTGCAGAGTGCTCATTTAAAATGCTAA 1439
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1141 CCTCAAGAGATGATTGATATTTGGTCTCAGTTGCAGAGTGCTCATTTAAAATGCTAA 1197

FIG. 9B

MSVGRRRIKLLGILMMANVFIYFIMEVSKSSSQEKNGKGEVIIPKEKFWKISTPPEAYWN
MSVGRRRIKLLGILMMANVFIYFIMEVSKSSSQEKNGKGEVIIPKEKFWKISTPPEAYWN
MSVGRRRIKLLGILMMANVFIYFIMEVSKSSSQEKNGKGEVIIPKEKFWKISTPPEAYWN

REQEKLNRQYNPILSMLTNQTGEAGRLSNISHLNYCEPDLRVTSVVTGFNNLPDRFKDFL
REQEKLNRQYNPILSMLTNQTGEAGRLSNISHLNYCEPDLRVTSVVTGFNNLPDRFKDFL
REQEKLNRQYNPILSMLTNQTGEAGRLSNISHLNYCEPDLRVTSVVTGFNNLPDRFKDFL

LYLRCRNYSLIDQPDKCAKKPFLLLAIKSLTPHFARRQAIRESWGQESNAGNQTVVRVF
LYLRCRNYSLIDQPDKCAKKPFLLLAIKSLTPHFARRQAIRESWGQESNAGNQTVVRVF
LYLRCRNYSLIDQPDKCAKKPFLLLAIKSLTPHFARRQAIRESWGQESNAGNQTVVRVF

LLGQTPPEDNHPDLSMLKFESEKHQDILMWNYRDTFFNLSLKEVLFLRWVSTSCPDEF
LLGQTPPEDNHPDLSMLKFESEKHQDILMWNYRDTFFNLSLKEVLFLRWVSTSCPDEF
LLGQTPPEDNHPDLSMLKFESEKHQDILMWNYRDTFFNLSLKEVLFLRWVSTSCPDEF

VFKGDDDFVFNTHHILNYLNSLSKTKAKDLFIGDVIHNAGPHRDKKLYYIPEVVYSGLY
VFKGDDDFVFNTHHILNYLNSLSKTKAKDLFIGDVIHNAGPHRDKKLYYIPEVVYSGLY
VFKGDDDFVFNTHHILNYLNSLSKTKAKDLFIGDVIHNAGPHRDKKLYYIPEVVYSGLY

PPYAGGGGFLYSGHLALRLYHITDQVHLYPIDDVYTMCLQKLGLVPEKHKGFRTFDIEE
PPYAGGGGFLYSGHLALRLYHITDQVHLYPIDDVYTMCLQKLGLVPEKHKGFRTFDIEE
PPYAGGGGFLYSGHLALRLYHITDQVHLYPIDDVYTMCLQKLGLVPEKHKGFRTFDIEE

KNKNNICSYVDLMLVHSRKPQEMIDIWSQLQSAHLKC
KNKNNICSYVDLMLVHSRKPQEMIDIWSQLQSAHLKC
KNKNNICSYVDLMLVHSRKPQEMIDIWSQLQSAHLKC

FIG. 10

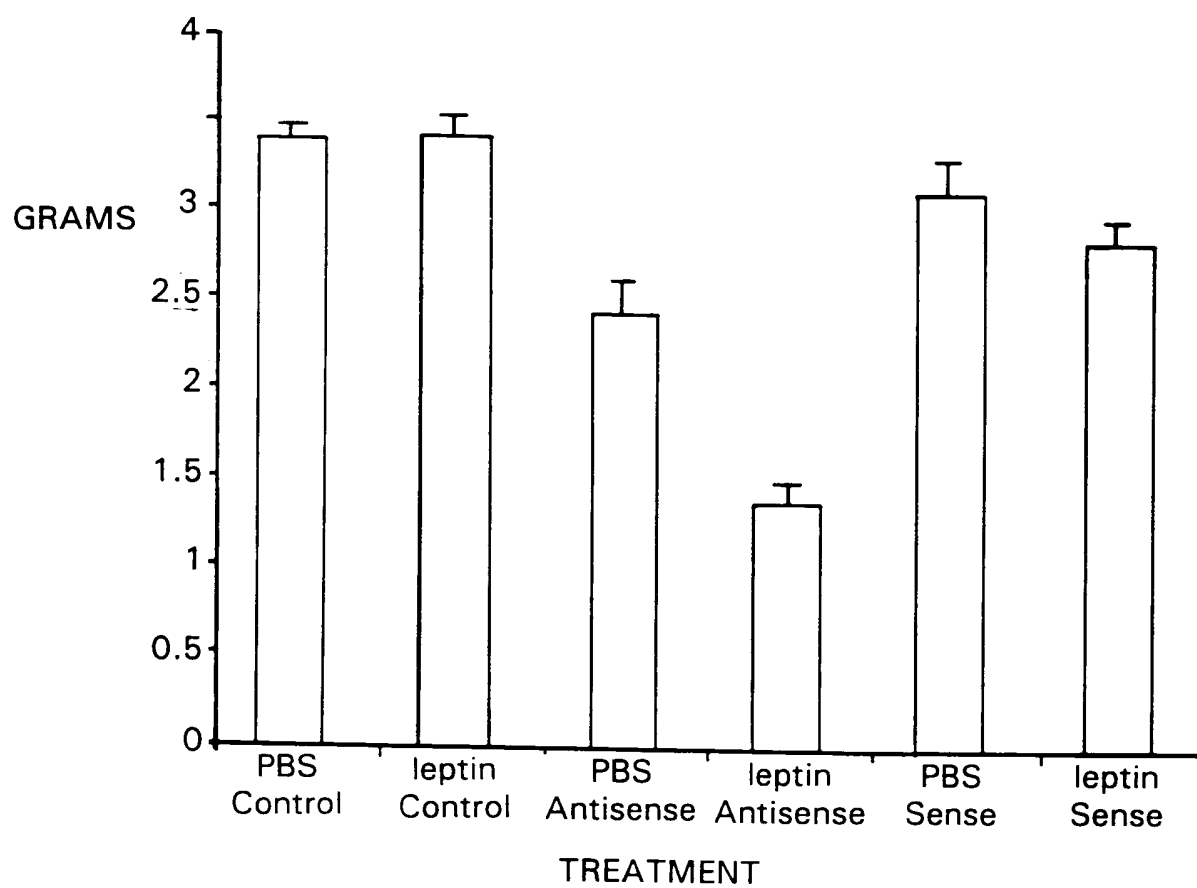


FIG. 11